sp   P00737   HPT1_	HUMAN N	MSALGAVIALLLWGQLFAVDS@MDVTDIADDGCPKPPEIAHGYVEHSVRYQCKNYYKLRT	60
sp P00738 HPT2_		MSALGAVIALLLWGQLFAVDSGNDVTDIADDGCPKPPEIAHGYVEHSVRYQCKNYYKLRT	60
sp   P50417   HPT_A	ATEGE N	MSALGAVIALLLWGQLFAVDSGNDVTDIADDGCPKPPEIANGYVEHLVRYQCKKYYRLRT	60
tr[Q60574 Q6057	74 P	MRALGAVVTLLLWGQLFAVELGNDAMDFEDDSCPKPPEIANGYVEHLVRYRCRQFYRLRA	60
tr Q61646 Q6164		MRALGAVVTLLLWGQLFAVELGNDAMDFEDDSCPKPPEIANGYVEHLVRYRCRQFYRLRA	60
sp   Q62558   HPT_M		MRALGAVVTLLLWGQLFAAELGNDAMDFEDDSCPKPPEIANGYVEHLVRYRCRQFYRLRT	60
sp   P06866   HPT_F		MRALGAVVTLLLWGQLFAVELGNDATDIEDDSCPKPPEIANGYVEHLVRYRCRQFYKLQT	50
tr 035086 03508		YRALGAVVTLLLWGQLFAVDLSNDAMDTADDSCPKPPEIENGYVEHLVRYRC-QHYRLRT	42
sp   P19006   HPT_C	CANFA -	::, : : . **** * :**** :**:* .*:*::	42
		1 1 1	
I need no large	THE MAN T	EGDGVYTLN	69
sp   P00737   HPT1_ sp   P00738   HPT2_		EGDGVYTLNDKKQWINKAVGDKLPECEADDGCPKPPEIAHGYVEHSVRYQCKNYYKLRTE	
sp   P50417   HPT_F		EGDGVYTLN	69
tr Q60574 Q6057		EGDGVYTLN	69
tr Q61646 Q6164	16 7	CCDGVYTIN	69
sp Q62558 HPT_N		EGDGVYTLN	69
sp   P06866   HPT_F		EGDGIYTLN	69
tr 035086 03508		EGDGVYTLN	
sp   P19006   HPT_C		EGDGVYTLN	51.
mp 1:23000 111-1		****:***	
sp   P00737   HPT1_	HUMAN -	nekqwinkavgdklpeceavcgkpknpanpvqrilgghldakgsfpwqakmv	121
sp   P00738   HPT2	HUMAN (	3DGVYTLNNEKQWINKAVGDKLPECEAVCGKPKNPANPVQRILGGHLDAKGSFPWQAKMV	180
sp P50417 HPT_	ATEGE -	nekowtnkavgdklpeceavcgkpknpanpvorilgghldakgsfpwoakmv	121
tr   Q60574   Q6057	74 -	DEKQWMNTVAGEKLPECEAVCGKPKHPVDQVQRIIGGSMDAKGSFPWQAKMI	121
tr   Q61646   Q6164	46	DEKQWVNTVAGEKLPECEAVCGKPKHPVDQVQRIIGGSMDAKGSFPWQAKMI	121
sp Q62558 HPT_N		DEKQWVNTAAGEKLPECEAVCGKPKHPVVQVQRIIGGSMDAKGSFPWQAKMI	121
sp   P06866   HPT_F		SEKQWVNPAAGDKLPKCEAVCGKPKHPVDQVQRIIGGSMDAKGSFPWQAKMI	121
tr 035086 03508		SEKQWVNTAAGERLPECEAVCGKPKHPVDQVQRIIGGSLDAKGSFPWQAKMV	120
sp   P19006   HPT_C	CANFA	SEKHWINKAVGEKLPECEAVCGKPKNPVDQVQRINGGSVDAKGSFPWQAKMV	103
		.**:* **::**:*******:*. ****:** :********	
I man o more l'arroma	THUMBER	SHHNLTTGATLINEQWLLTTAKNLFLNHSENATAKDIAPTLTLYVGKKQLVEIEKVVLHP	181
sp   P00737   HPT1_ sp   P00738   HPT2		SHHNLTTGATLINEQWILLTTAKNIFINHSENATAKDIAPTLTLYVGKKQLVEIEKVVLHP	240
		srenit toktitikegyllitaknifinesenatakdiaptitilyvgknolveiekvvlyp	181
sp   P50417   HPT_3 tr   Q60574   Q6057		SRHGLTTGATLISDOWLLTTAKNLFLNHSETASGKDIAPTLTLYVGKNOLVEIEKVILHP	181
tr 061646 Q6164		SRHGLTTGATLISDQWLLTTAKNLFLNHSETASAKDITPTLTLYVGKNQLVEIEKVVLHP	
sp   Q62558   HPT_1		SRHGLTTGATLISDQWLLTTAKNLFLNHSETASAKDIAPTLTLYVGKNQLVEIEKVVLHP	181
sp   P06866   HPT_I		SRHGLTTGATLISDQWLLTTAQNLFLNHSENATAKDIAPTLTLYVGKNQLVEIEKVVLHP	181
tr   035086   0350		SRHELITGATLISDQWLLTTAKNLFLNHSEDATSKDIAPTLKLYVGKMQPVEIEKVVIHP	180
sp   P19006   HPT_C	CANFA	SHHNLTSGATLINEOWLLTTAKNLFLGHKDDAKANDIAPTLKLYVGKNQLVEVEKVVLHP	163
ablinaced in		*:* * :***** * :***** * :*** * ::**:**	
sp   P00737   HPT1	HUMAN	nysovdigliklkokvsvnervmpiclpskdyaevgrvgyvsgwgrnanfkftdhlkyvm	241
sp   P00738   HPT2	HUMAN	nysovdigliklkokvsvnervmpiclpskdyaevgrvgyvsgwgrnanfkftdhlkyvm	300
sp   P50417   HPT_	ATEGE	nysqvdigliklkdkvpvnervmpiclpskdyaevgrvgyvsgwgrnanfkftdhlkyvm	241
tr   Q60574   Q605	74	${\tt NHSVVDIGLIKLKQRVLVTERVMPICLPSKDYVAPGRVGYVSGWGRNQDFRFTDRLKYVM}$	241
tr Q61646 Q616		NHSVVDIGLIKLKQRVLVTERVMPICLPSKDYIAPGRVGYVSGWGRNANFRFTDRLKYVM	241
sp   Q62558   HPT_I	MUSSA	NHSVVDIGLIKLKQRVLVTERVMPICLPSKDYVAPGRVGYLSGWGRNVNFRFTERFKYVM	241
sp   P06866   HPT_1	RAT	ERSVVDIGLIKLKQKVLVTEKVMPICLPSKDYVAPGRMGYVSGWGRNVNFRFTERLKYVM	241
tr 035086 0350		NRSVVDIGVIKLROKVPVNERVMPICLPSKDYIAPGRMGYVSGWGRNANFRFTDRLKYVM	240
sp   P19006   HPT_	CANFA	DYSKVDIGLIKLKQKVPIDER VMPICLPSKDYAEVGRIGYVSGWGRNSNFNFTELLKYVM	223
		: * ****:***:::* : *:*********	
	THIMAN	LPVADQDQCIRHYEGSTVPEKKTPKSPVGVQPILMEHTFCAGMSKYQEDTCYGDAGSAFA	301
sp P00737 HPT1		LPVADQDQCIRHYEGSTVPEKKTPKSPVGVQFILMEHTFCAGMSKYQEDTCYGDAGSAFA LPVADQDQCIRHYEGSTVPEKKTPKSPVGVQFILMEHTFCAGMSKYQEDTCYGDAGSAFA	360
sp   P00738   HPT2		LPVADQVQCVKHYEGSTVPEKKTPKSPVGVQFILMEHTFCAGMSKYQEDTCYGDAGSAFA	301
sp   P50417   HPT_		LPVADQDKCVVHYEKSTVPEKKNFTSPVGVQPILNEHTFCAGLTKYEEDTCYGDAGSAFA	301
tr Q60574 Q605	14	LPVADQDKCVVHYENSTVPEKKNLTSPVGVQFILNEHTFCAGLTKYQEDTCYGDAGSAFA	301
tr Q61646 Q616		LPVADQDKCVVHYENSTVPEKKNFTSPVGVQPILNEHTFCVGLSRYQEDTCYGDAGSAFA	301
sp   Q62558   HPT_ sp   P06866   HPT_		LPVADQEKCELHYEKSTVPEKKGAVTPVGVQPILNKHTFCAGLTKYEEDTCYGDAGSAFA	301
tr 035086 0350		LPVADQDSCMLHYEGSTVPEKEGSKSSVGVQPILMEHTFCAGMTKYQEDTCYGDAGSAFA	300
8D P19006 HPT		LPVADQDKCVQHYEGSTVPEKKSPKSPVGVQPILNEHTFCAGMSKFQEDTCYGDAGSAFA	283
Phirrange   Hhr."	-watt A	***** .* *** ****** : :.** ****:***.*:::::********	

## Figure 4b

ep P00737 HPT1_HUMAN sp P00738 HFT2_HUMAN sp P50417 HPT_ATEGE tr Qe0574 Q60574 tr Qe1646 Qe1646 sp Qe2528 HTP_MUSSA sp P06866 HPT_RAT tr Q53086 Q35086 sp P190086 HTP_CANFA	VHDLEEDTWYATGILSFDKSCAVAI VHDLEEDTWYATGILSFDKSCAVAI VHDLEEDTWYAAGILSFDKSCAVAI IHDMEDTWYAAGILSFDKSCAVAI IHDMEDTWYAAGILSFDKSCAVAI IHDMEDTWYAAGILSFDKSCAVAI IHDMEDTWYAAGILSFDKSCAVAI IHDLEOTWYAAGILSFDKSCAVAI IHDLEOTWYAAGILSFDKSCAVAI VHDDEDTWYAAGILSFDKSCAVAI VHDDEDTWYAAGILSFDKSCAVAI IHDLEOTWYAAGILSFDKSCAVAI IHDLEOTWYAAGILSFDK
BD   PI 3000   HI I CAMIN	

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VIBILEDTYMATOLISPINGAVARYGUVYVATTSIODMUKATIAEN 347
VIBILEDTYMATOLISPINGAVARYGUVYVATTSIODMUKATIAEN 347
VIBILEDTYMATOLISPINGAVARYGUVYVATTSIODMUKATIAEN 347
VIBILEDTYMATOLISPINGAVARYGUVYARTSIODMUKATIAEN 347
VIBINGEDTYMATOLISPINGAVARYGUVYARTOLIKOWOGENTAKN 347
VIBINSEDTYMATOLISPINGAVARYGUVYARTOLIKOWOGENTAKN 347
VIBINSEDTYMATOLISPINGAVARYGUVYVARTOLIKOWOGENTAKN 347
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		MVLLEDSGSADFRRHFVNLSPFTITVVLLLSACFVTSSLGGTDKELRLVDGENKCSGRVE 6	0
CD163	-	MVLLEDSGSADFRRHFVNLSPFTITVVLLLSACFVTSSLGGTDKELRLVDGENKCSGRVE	60
CD163 cyt. Var		MVLLEDSGSADFRRHFVNLSPFTITVVLLLSACFVTSSLGGTDKELRLVDGENKCSGRVE	60
CD163 cyt. var CD163 ext. cell	17		60
CD163 exc. deli	. Vall.	***************	
tr Q07898 Q0789	8	VKVQEEWGTVCNNGWSMEAVSVICNQLGCPTAIKAPGWANSSAGSGRIWMDHVSCRGNES	120
tr   Q07901   Q0790			
tr Q07900 Q0790		VKVQEEWGTVCNNGWSMEAVSVICNQLGCPTAIKAPGWANSSAGSGRIWMDHVSCRGNES	120
tr Q07899 Q0789	9	VKVQEEWGTVCNNGWSMEAVSVICNQLGCPTAIKAPGWANSSAGSGRIWMDHVSCRGNES	120
		********************************	
tr Q07898 Q0789	8	$\verb ALWDCKHDGWGKHSNCTHQQDAGVTCSDGSNLEMRLTRGGNMCSGRIEIKFQGRWGTVCD \\$	180
tr   Q07901   Q0790		ALWDCKHDGWGKHSNCTHQQDAGVTCSDGSNLEMRLTRGGNMCSGRIE1KFQGRWGTVCD	180
tr   Q07900   Q0790		ALWDCKHDGWGKHSNCTHQQDAGVTCSDGSNLEMRL/TRGGNMCSGRIEIKFQGRWGTVCD	180
tr Q07899 Q0789	9	ALWDCKHDGWGKHSNCTHQQDAGVTCSDGSNLEWRLTRGGNMCSGRIEIKFQGRWGTVCD	180
		*************	
tr 007898 Q0789	8	DNFNIDHASVICROLECGSAVSFSGSSNFGEGSGPIWFDDLICNGNESALWNCKHQGWGK	240
tr Q07901 Q0790		DNFNIDHASVICRQLECGSAVSFSGSSNFGEGSGPIWFDDLICNGNESALWNCKHQGWGK	240
tr  Q07900  Q0790	0	DNFNI DHASVI CRQLECGSAVSFSGSSNFGEGSGPIWFDDLI CNGNESALWNCKHQGWGK	240
tr   Q07899   Q0789		DNFNIDHASVICRQLECGSAVSFSGSSNFGEGSGPIWFDDLICNGNESALWNCKHQGWGK	240
C1   Q0 /03 5   Q0 /03	-	**************	
		HNCDHAEDAGVICSKGADLSLRLVDGVTECSGRLEVRFQGEWGTICDDGWDSYDAAVACK	300
tr Q07898 Q0789		HNCDHAEDAGVICSKGADLSLRLVDGVTECSGRLEVRFQGEWGTICDDGWDSYDAAVACK	300
tr Q07901 Q0790		HNCDHAEDAGVICSKGADLSLRLVDGVTECSGRLEVRFQGEWGTICDDGWDSYDAAVACK	300
tr Q07900 Q0790		ENCOMAEDAGVICSKGADLSLENDGVIECSGRLEVRFQGEWGTICDDGWDSYDAAVACK	300
tr Q07899 Q0789	,	******************	
		THE PROPERTY OF THE PROPERTY O	350
tr   Q07898   Q0789		QLGCPTAVTA I GRVNAS KGFGHI WLDSVSCQGHEPAVWQCKHHEWGKHYCNHNEDAGVTC QLGCPTAVTA I GRVNAS KGFGHI WLDSVSCQGHEPAVWQCKHHEWGKHYCNHNEDAGVTC	360
tr Q07901 Q0790		QLGCPTAVTAIGRVNASKGFGHIWLDSVSCQGHEPAVWQCKHHEWGKHYCNHNEDAGVTC	360
tr   Q07900   Q0790		QLGCPTAVTAIGRVNASKGFGHIWLDSVSCQGHEPAVWQCKHHEWGKHYCNHNEDAGVTC	360
tr Q07899 Q0789	9	**************************************	
		SDGSDLELRLRGGGSRCAGTVEVEIQRLLGKVCDRGWGLKEADVVCRQLGCGSALKTSYQ	420
tr Q07898 Q0789		SDGSDLELRLRGGGSRCAGTVEVEIQRLLGKVCDRGWGLKEADVVCRQLGCGSALKTSYQ	420
tr   Q07901   Q0790		SDGSDLELRLRGGGSRCAGTVEVEIQRLLGKVCDRGWGLKEADVVCRQLGCGSALKTSYQ	420
tr Q07900 Q0790		SDGSDLELRLRGGGSRCAGTVEVEIQRLLGKVCDRGWGLKEADVVCRQLGCGSALKTSYQ	420
tr Q07899 Q0789	9	**************	
		THE PROPERTY OF THE PROPERTY O	480
tr  Q07898  Q0789		VYSKIQATNTWLFLSSCNGNETSLWDCKNWQWGGLTCDHYEEAKITCSAHREPRLVGGDI VYSKIQATNTWLFLSSCNGNETSLWDCKNWQWGGLTCDHYEEAKITCSAHREPRLVGGDI	480
tr   207901   20790		VYSKIQATNTWLFLSSCNGNETSLWDCKNWQWGGLTCDHYEEAKITCSAHREPRLVGGDI	480
tr   Q07900   Q0790		VYSKIQATNIWLFLSSCNGNEISLWDCKNWQWGGLTCDHYEEAKITCSAHREPRLVGGDI	480
tr Q07899 Q0789	19	**************************************	
			E40
tr Q07898 Q0789		PCSGRVEVKHGDTWGSICDSDFSLEAASVLCRELQCGTVVSILGGAHFGEGNGQIWAEEF	540
tr Q07901 Q0790		PCSGRVEVKHGDTWGSICDSDFSLEAASVLCRELQCGTVVSILGGAHFGEGNGQIWAEEF	540
tr Q07900 Q0790		PCSGRVEVKHGDTWGSICDSDFSLEAASVLCRELQCGTVVSILGGAHFGEGNGQIWAEEF	540
tr Q07899 Q0785	19	PCSGRVEVKHGDTWGSICDSDFSLEAASVLCRELQCGTVVSILGGAHFGEGNGQIWAEEF	540
tr Q07898 Q0789		QCEGHESHLSLCPVAPRPEGTCSHSRDVGVVCS	573
tr Q07901 Q0790		QCEGHESHLSLCPVAPRPEGTCSHSRDVGVVCSSKTQKTSLIGSYTVKGTGLGSHSCLFL	600
tr Q07900 Q0790		QCEGHESHLSLCPVAPRPEGTCSHSRDVGVVCS	5/3
tr Q07899 Q0789	99	QCEGHESHLSLCPVAPRPEGTCSHSRDVGVVCS	5/3
tr  Q07898  Q078	98	RYTEIRLVNGKTPCEGRVELKTLGAWGSLCNSHWDIEDAHVLCQQLKCGVALST	627
tr Q07901 Q0790		KPCLLPGYTEIRLVNGKTPCBGRVELKTLGAWGSLCNSHWDIEDAHVLCQQLKCGVALST	660
tr  Q07900  Q079	0.0	RYTEIRLVNGKTPCEGRVELKTLGAWGSLCNSHWDIEDAHVLCQQLKCGVALST	627
tr Q07899 Q078	99	RYTEIRLVNGKTPCEGRVELKTLGAWGSLCNSHWDIEDAHVLCQQLKCGVALST	627
		************	